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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2009; month=2; day=19; hr=10; min=35; sec=1; ms=967;]

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Reviewer Comments:

<220>

<221> VARIANT

<222> (297)...(297)

<223> tyrosine, valine, isoleucine, leucine, methionine, phenylalanine, tryptophan

<400> 6

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1				5					10					15	
Xaa	Gln	Xaa	Xaa	Glu	Xaa	Xaa	Xaa	Xaa	Leu	Leu	Leu	Xaa	Xaa	Xaa	Xaa
			20					25						30	
Gly	Xaa	Xaa	Xaa	Phe	Xaa	Val	Xaa	Pro	Xaa	Val	Gly	Xaa	Gly	Gly	Xaa
			35					40						45	

A mandatory feature is required to cover every "Xaa" used in a sequence. SEQ ID # 6 does not have a feature to cover the "Xaa" at positions 223. Please make all necessary changes.

Application No: 10573372 Version No: 2.0

Input Set:

Output Set:

Started: 2009-01-30 19:08:24.415
Finished: 2009-01-30 19:08:35.769
Elapsed: 0 hr(s) 0 min(s) 11 sec(s) 354 ms
Total Warnings: 5
Total Errors: 4
No. of SeqIDs Defined: 7
Actual SeqID Count: 7

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (6)
E 341	'Xaa' position not defined SEQID (6) POS (223)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (7)

<110> Dale, James Langham
Echeverria, Santy Peraza

<130> DAVI172.006APC

<141> 2009-01-30

<151> 2004-09-23

<151> 2003-09-25

<170> FastSEQ for Windows Version 4.0

<211> 4380

<212> DNA

<213> Musa acuminata

 $\langle 220 \rangle$

<221> CDS

$\langle 222 \rangle$ (1) . . (4323)

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1 5 10 15

cag acg ttg ctc gac aag gcc agc aac tgc gcg atc caa caa ctc gcg 96
Gln Thr Leu Leu Asp Lys Ala Ser Asn Cys Ala Ile Gln Gln Leu Ala
20 25 30

cgg cgc cgc ggc ctt cac gat gac ctg agg cgg ctg cgg acg tct ctg 144
Arg Arg Arg Gly Leu His Asp Asp Leu Arg Arg Leu Arg Thr Ser Leu
35 40 45

ctc cgg atc cat gcc atc ctc gac aag gca gag acg agg tgg aac cat 192
Leu Arg Ile His Ala Ile Leu Asp Lys Ala Glu Thr Arg Trp Asn His
50 55 60

aaa aac acg agc ttg gtg gag ctg gtg agg cag ctc aag gat gct gcc 240
Lys Asn Thr Ser Leu Val Glu Leu Val Arg Gln Leu Lys Asp Ala Ala
65 70 75 80

tat gac gcc gag gac tta ctg gag gag ttg gag tac caa gcc gcg aag 288

Tyr Asp Ala Glu Asp Leu Leu Glu Glu Leu Glu Tyr Gln Ala Ala Lys	
85 90 95	
caa aag gtc gag cac cgg gga gac cag ata agc gac ctc ttt tct ttt	336
Gln Lys Val Glu His Arg Gly Asp Gln Ile Ser Asp Leu Phe Ser Phe	
100 105 110	
tcc ctt agt act gcg agc gag tgg ttg ggt gcc gat ggt gat gat gct	384
Ser Leu Ser Thr Ala Ser Glu Trp Leu Gly Ala Asp Gly Asp Asp Ala	
115 120 125	
ggg act cga ttg agg gag atc cag ggg aag ctg tgc aac att gct gcc	432
Gly Thr Arg Leu Arg Glu Ile Gln Gly Lys Leu Cys Asn Ile Ala Ala	
130 135 140	
gat atg atg gat gtc atg cag cta ttg gca ccc gat gat ggg ggg aga	480
Asp Met Met Asp Val Met Gln Leu Leu Ala Pro Asp Asp Gly Gly Arg	
145 150 155 160	
caa ttc gac tgg aag gtg gtg aga aga gaa acg agc tct ttc ttg acc	528
Gln Phe Asp Trp Lys Val Val Arg Arg Glu Thr Ser Ser Phe Leu Thr	
165 170 175	
gaa acc gtc gtg ttt ggt cgg gac caa gaa agg gag aaa gta gta gaa	576
Glu Thr Val Val Phe Gly Arg Asp Gln Glu Arg Glu Lys Val Val Glu	
180 185 190	
ttg ctg ttg gat tca gga tct ggt aac agt agc ttc tct gtc tta ccc	624
Leu Leu Leu Asp Ser Gly Ser Gly Asn Ser Ser Phe Ser Val Leu Pro	
195 200 205	
ctc gtc gga atc gga ggg gtt ggg aag acg act ctg gct cag ctc gtg	672
Leu Val Gly Ile Gly Gly Val Gly Lys Thr Thr Leu Ala Gln Leu Val	
210 215 220	
tac aac gac aat cgt gtc ggc aac tat ttc cac ctc aag gtt tgg gtc	720
Tyr Asn Asp Asn Arg Val Gly Asn Tyr Phe His Leu Lys Val Trp Val	
225 230 235 240	
tgt gta tcc gac aat ttc aat gtg aag aga ctg acc aaa gag ata atc	768
Cys Val Ser Asp Asn Phe Asn Val Lys Arg Leu Thr Lys Glu Ile Ile	
245 250 255	
gag tct gct acc aag gtg gaa caa tct gac aaa ttg aac ttg gac acc	816
Glu Ser Ala Thr Lys Val Glu Gln Ser Asp Lys Leu Asn Leu Asp Thr	
260 265 270	
ctg caa cag atc ctc aag gag aag att gct tca gag agg ttt ctg cta	864
Leu Gln Gln Ile Leu Lys Glu Lys Ile Ala Ser Glu Arg Phe Leu Leu	
275 280 285	
gtc ctc gat gat gtg tgg agc gaa aac agg gat gac tgg gaa agg ctg	912
Val Leu Asp Asp Val Trp Ser Glu Asn Arg Asp Asp Trp Glu Arg Leu	
290 295 300	
tgc gca cca cta agg ttt gca gca aga ggc agc aag gtt ata gtc aca	960
Cys Ala Pro Leu Arg Phe Ala Ala Arg Gly Ser Lys Val Ile Val Thr	

305	310	315	320	
act cga gac aca aag att gcc agc atc att ggc aca atg aag gaa att				1008
Thr Arg Asp Thr Lys Ile Ala Ser Ile Ile Gly Thr Met Lys Glu Ile				
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tcg ctc gat ggt ctc cag gat gat gct tac tgg gag ctg ttc aag aaa				1056
Ser Leu Asp Gly Leu Gln Asp Asp Ala Tyr Trp Glu Leu Phe Lys Lys				
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tgt gca ttt ggt tct gtg aac ccc cag gag cat cta gag ctc gag gtt				1104
Cys Ala Phe Gly Ser Val Asn Pro Gln Glu His Leu Glu Leu Glu Val				
	355	360	365	
atc ggt aga aag att gct ggt aag ttg aag ggc tca ccg cta gca gca				1152
Ile Gly Arg Lys Ile Ala Gly Lys Leu Lys Gly Ser Pro Leu Ala Ala				
	370	375	380	
aaa aca cta gga agc ttg ttg cgg ttg gat gtc agc caa gaa cac tgg				1200
Lys Thr Leu Gly Ser Leu Leu Arg Leu Asp Val Ser Gln Glu His Trp				
	385	390	395	400
aga act ata atg gaa agt gag gta tgg caa ctg cca caa gct gaa aat				1248
Arg Thr Ile Met Glu Ser Glu Val Trp Gln Leu Pro Gln Ala Glu Asn				
	405	410	415	
gaa ata ttg cct gtt cta tgg ctg agc tat caa cac ctt ccc gga cat				1296
Glu Ile Leu Pro Val Leu Trp Leu Ser Tyr Gln His Leu Pro Gly His				
	420	425	430	
ctt aga cag tgt ttc gct ttt tgc gct gtg ttt cac aaa gat tat tta				1344
Leu Arg Gln Cys Phe Ala Phe Cys Ala Val Phe His Lys Asp Tyr Leu				
	435	440	445	
ttc tat aaa cat gag ttg atc cag act tgg att gca gaa ggc ttc att				1392
Phe Tyr Lys His Glu Leu Ile Gln Thr Trp Ile Ala Glu Gly Phe Ile				
	450	455	460	
gca cat caa gga aac aag agg atg gaa gat gtc gga agc agc tac ttc				1440
Ala His Gln Gly Asn Lys Arg Met Glu Asp Val Gly Ser Ser Tyr Phe				
	465	470	475	480
cat gag ctt gtt aat agg tct ttc ttt cag gaa tct cgg tgg aga ggg				1488
His Glu Leu Val Asn Arg Ser Phe Phe Gln Glu Ser Arg Trp Arg Gly				
	485	490	495	
cga tat gtg atg cat gac ctc ata cac gat ctt gcc caa ttt ata tca				1536
Arg Tyr Val Met His Asp Leu Ile His Asp Leu Ala Gln Phe Ile Ser				
	500	505	510	
gtg gga gag tgt cat agg ata gat gat gac aag tcc aaa gag acc cct				1584
Val Gly Glu Cys His Arg Ile Asp Asp Asp Lys Ser Lys Glu Thr Pro				
	515	520	525	
agt acg act cgt cat cta tca gta gca tta act gag caa atg aag ttg				1632
Ser Thr Thr Arg His Leu Ser Val Ala Leu Thr Glu Gln Met Lys Leu				
	530	535	540	

gtg	gat	ttt	tca	ggg	tac	aat	aaa	ttg	cgg	acc	ctt	atg	atc	aac	aat	1680
Val	Asp	Phe	Ser	Gly	Tyr	Asn	Lys	Leu	Arg	Thr	Leu	Met	Ile	Asn	Asn	
545			550			555			560							
cag	aga	aat	cag	tat	cca	tat	atg	act	aaa	gtc	aac	agc	tgc	ttg	ttg	1728
Gln	Arg	Asn	Gln	Tyr	Pro	Tyr	Met	Thr	Lys	Val	Asn	Ser	Cys	Leu	Leu	
565			570			575										
cct	cat	agc	ttg	ttc	aaa	aga	ctg	aaa	aga	atc	cat	gtt	tta	gtt	ttg	1776
Pro	His	Ser	Leu	Phe	Lys	Arg	Leu	Lys	Arg	Ile	His	Val	Leu	Val	Leu	
580			585			590										
cag	aag	tgt	ggc	atg	aaa	gag	ttg	cct	gat	att	atc	ggg	gac	ttg	ata	1824
Gln	Lys	Cys	Gly	Met	Lys	Glu	Leu	Pro	Asp	Ile	Ile	Gly	Asp	Leu	Ile	
595			600			605										
caa	ctt	cgg	tac	ctt	gac	ata	tcc	tac	aat	gct	tgc	att	cag	agg	ttg	1872
Gln	Leu	Arg	Tyr	Leu	Asp	Ile	Ser	Tyr	Asn	Ala	Cys	Ile	Gln	Arg	Leu	
610			615			620										
ccc	gag	tca	ttg	tgc	gac	ctt	tac	aat	ctg	caa	gca	ctg	agg	cta	tgg	1920
Pro	Glu	Ser	Leu	Cys	Asp	Leu	Tyr	Asn	Leu	Gln	Ala	Leu	Arg	Leu	Trp	
625			630			635			640							
ggc	tgt	caa	tta	cgg	agt	ttc	cca	caa	ggc	atg	agc	aag	ctg	atc	aac	1968
Gly	Cys	Gln	Leu	Arg	Ser	Phe	Pro	Gln	Gly	Met	Ser	Lys	Leu	Ile	Asn	
645			650			655										
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Leu	Arg	Gln	Leu	Arg	Val	Glu	Asp	Glu	Ile	Ile	Ser	Lys	Ile	Tyr	Glu	
660			665			670										
gtt	ggg	aag	ctg	att	tct	ctg	caa	gaa	ttg	tct	gca	ttc	aaa	gtg	cta	2064
Val	Gly	Lys	Leu	Ile	Ser	Leu	Gln	Glu	Leu	Ser	Ala	Phe	Lys	Val	Leu	
675			680			685										
aat	aat	cat	gga	aac	aaa	ctt	gca	gaa	cta	agt	ggg	ttg	aca	caa	ctc	2112
Asn	Asn	His	Gly	Asn	Lys	Leu	Ala	Glu	Leu	Ser	Gly	Leu	Thr	Gln	Leu	
690			695			700										
cgc	agc	act	cta	cga	att	aca	aat	ctt	gaa	aat	gta	ggg	agt	aaa	gaa	2160
Arg	Ser	Thr	Leu	Arg	Ile	Thr	Asn	Leu	Glu	Asn	Val	Gly	Ser	Lys	Glu	
705			710			715			720							
gaa	gca	agc	aag	gct	aaa	ctg	cac	agg	aaa	cag	tat	ctt	gaa	gca	tta	2208
Glu	Ala	Ser	Lys	Ala	Lys	Leu	His	Arg	Lys	Gln	Tyr	Leu	Glu	Ala	Leu	
725			730			735										
gag	tta	gag	tgg	gca	gct	ggc	cag	gtt	tcc	agc	ttg	gag	cat	gag	tta	2256
Glu	Leu	Glu	Trp	Ala	Ala	Gly	Gln	Val	Ser	Ser	Leu	Glu	His	Glu	Leu	
740			745			750										
ctt	gtc	tcg	gag	gaa	gta	ctt	tta	ggg	ctc	caa	cca	cat	cac	ttc	ctc	2304
Leu	Val	Ser	Glu	Glu	Val	Leu	Leu	Gly	Leu	Gln	Pro	His	His	Phe	Leu	
755			760			765										

aaa agt ttg aca atc aga ggg tac agt ggt gca aca gta ccc agt tgg	2352
Lys Ser Leu Thr Ile Arg Gly Tyr Ser Gly Ala Thr Val Pro Ser Trp	
770 775 780	
ctg gat gtg aaa atg cta ccg aac ttg gga act ctt aaa cta gag aac	2400
Leu Asp Val Lys Met Leu Pro Asn Leu Gly Thr Leu Lys Leu Glu Asn	
785 790 795 800	
tgt aca aga ctg gag ggt ctt tca tat att gga caa ctg cca cat ctc	2448
Cys Thr Arg Leu Glu Gly Leu Ser Tyr Ile Gly Gln Leu Pro His Leu	
805 810 815	
aag gtc ctt cat atg aag aga atg cct gtg gtg aaa caa atg agt cat	2496
Lys Val Leu His Met Lys Arg Met Pro Val Val Lys Gln Met Ser His	
820 825 830	
gaa tta tgt ggc tgt acg aaa agc aag ttg ttc cct agg cta gaa gag	2544
Glu Leu Cys Gly Cys Thr Lys Ser Lys Leu Phe Pro Arg Leu Glu Glu	
835 840 845	
tta gta ctg gag gat atg cca aca ttg aaa gaa ttc ccg aat ctt gca	2592
Leu Val Leu Glu Asp Met Pro Thr Leu Lys Glu Phe Pro Asn Leu Ala	
850 855 860	
caa ctt cct tgt ctc aag att att cac atg aag aac atg ttt gca gta	2640
Gln Leu Pro Cys Leu Lys Ile Ile His Met Lys Asn Met Phe Ala Val	
865 870 875 880	
aaa cat ata ggt cgt gaa tta tat ggt gat ata gag agc aat tgt ttt	2688
Lys His Ile Gly Arg Glu Leu Tyr Gly Asp Ile Glu Ser Asn Cys Phe	
885 890 895	
cta tca tta gaa gag ctt gtg ctg cag gac atg ctg aca ttg gag gaa	2736
Leu Ser Leu Glu Glu Leu Val Leu Gln Asp Met Leu Thr Leu Glu Glu	
900 905 910	
ctc cca aat ctt gga caa ctt cca cat ctt aag gtt att cac atg aag	2784
Leu Pro Asn Leu Gly Gln Leu Pro His Leu Lys Val Ile His Met Lys	
915 920 925	
aac atg tct gca ctg aaa ctt ata ggt cgt gaa tta tgt gat tct aga	2832
Asn Met Ser Ala Leu Lys Leu Ile Gly Arg Glu Leu Cys Asp Ser Arg	
930 935 940	
gag aaa att tgg ttt cct agg cta gaa gtg cta gtg ctg aag aac atg	2880
Glu Lys Ile Trp Phe Pro Arg Leu Glu Val Leu Val Leu Lys Asn Met	
945 950 955 960	
ctg gca ctg gag gaa ctc cca agc ttg gac aac ttc cgt gtc tca aga	2928
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965 970 975	
ttc ttc gca tcc agt gtc gaa gta ggc cat gga ctc ttt agt gct acg	2976
Phe Phe Ala Ser Ser Val Glu Val Gly His Gly Leu Phe Ser Ala Thr	
980 985 990	
agg aat aaa tgg ttt cca agg ctg gaa gag cta gaa atc aag ggc atg	3024

Arg	Asn	Lys	Trp	Phe	Pro	Arg	Leu	Glu	Glu	Leu	Glu	Ile	Lys	Gly	Met	
995							1000			1005						
ctg	aca	ttt	gag	gaa	ctc	cat	tct	ctt	gaa	aaa	ctg	cca	tgt	ctc		3069
Leu	Thr	Phe	Glu	Glu	Leu	His	Ser	Leu	Glu	Lys	Leu	Pro	Cys	Leu		
1010		1015					1020									
aag	gtt	ttc	cgc	atc	aag	gga	ttg	cca	gca	gtg	aaa	aag	ata	ggc		3114
Lys	Val	Phe	Arg	Ile	Lys	Gly	Leu	Pro	Ala	Val	Lys	Lys	Ile	Gly		
1025		1030					1035									
cat	gga	tta	ttt	gat	tct	acc	tgt	cag	aga	gag	tgt	ttt	cca	agg		3159
His	Gly	Leu	Phe	Asp	Ser	Thr	Cys	Gln	Arg	Glu	Cys	Phe	Pro	Arg		
1040		1045					1050									
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Leu	Glu	Asp	Leu	Val	Leu	Ser	Asp	Met	Pro	Ala	Trp	Glu	Glu	Trp		
1055		1060					1065									
tcg	tgg	gct	gaa	agg	gag	gag	tta	ttt	tcc	tgc	ttg	tgt	aga	ctt		3249
Ser	Trp	Ala	Glu	Arg	Glu	Glu	Leu	Phe	Ser	Cys	Leu	Cys	Arg	Leu		
1070		1075					1080									
aaa	att	gaa	caa	tgc	ccc	aaa	ctt	aaa	tgc	ttg	ctt	ccc	atc	cct		3294
Lys	Ile	Glu	Gln	Cys	Pro	Lys	Leu	Lys	Cys	Leu	Leu	Pro	Ile	Pro		
1085		1090					1095									
cat	tct	ctc	ata	aaa	ctt	gaa	tta	tgg	caa	gtt	ggg	ctg	aca	gga		3339
His	Ser	Leu	Ile	Lys	Leu	Glu	Leu	Trp	Gln	Val	Gly	Leu	Thr	Gly		
1100		1105					1110									
ctt	cca	gga	tta	tgc	aaa	gga	att	ggt	gga	ggt	agc	agc	act	aga		3384
Leu	Pro	Gly	Leu	Cys	Lys	Gly	Ile	Gly	Gly	Gly	Ser	Ser	Thr	Arg		
1115		1120					1125									
act	gct	tct	ctc	tca	ctc	ttg	cac	att	att	aaa	tgt	cca	aat	ctg		3429
Thr	Ala	Ser	Leu	Ser	Leu	Leu	His	Ile	Ile	Lys	Cys	Pro	Asn	Leu		
1130		1135					1140									
aga	aat	ctg	gga	gaa	ggg	ttg	cta	tca	aac	cac	ctg	cca	cat	atc		3474
Arg	Asn	Leu	Gly	Glu	Gly	Leu	Leu	Ser	Asn	His	Leu	Pro	His	Ile		
1145		1150					1155									
aat	gct	att	cgg	ata	tgg	gaa	tgt	gct	gaa	ctg	ttg	tgg	ctg	cct		3519
Asn	Ala	Ile	Arg	Ile	Trp	Glu	Cys	Ala	Glu	Leu	Leu	Trp	Leu	Pro		
1160		1165					1170									
gtc	aag	agg	ttt	aga	gaa	ttc	acc	acc	ctt	gag	aac	ttg	tca	ata		3564
Val	Lys	Arg	Phe	Arg	Glu	Phe	Thr	Thr	Leu	Glu	Asn	Leu	Ser	Ile		
1175		1180					1185									
agg	aac	tgc	ccc	aag	ctc	atg	agc	atg	aca	cag	tgt	gag	gag	aat		3609
Arg	Asn	Cys	Pro	Lys	Leu	Met	Ser	Met	Thr	Gln	Cys	Glu	Glu	Asn		
1190		1195					1200									
gac	ctc	ctc	ctc	ccg	ccg	tta	atc	aag	gca	cta	gaa	ttg	ggt	gac		3654
Asp	Leu	Leu	Leu	Pro	Pro	Leu	Ile	Lys	Ala	Leu	Glu	Leu	Gly	Asp		

1205

1210

1215

tgt gga aat ctt ggg aaa tcg ctg cct gga tgc cta